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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/925,664

DATE: 03/05/2001

TIME: 14:00:50

Input Set : A:\06499-1.txt

Output Set: N:\CRF3\03052002\I925664.raw

3 <110> APPLICANT: Denney, Jr., Dan W.
 5 <120> TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
 7 <130> FILE REFERENCE: GENITOP-06499
 9 <140> CURRENT APPLICATION NUMBER: 09/925,664
 10 <141> CURRENT FILING DATE: 2001-08-09
 12 <150> PRIOR APPLICATION NUMBER: 09/370,453
 13 <151> PRIOR FILING DATE: 1999-08-09
 15 <150> PRIOR APPLICATION NUMBER: 08/644,664
 16 <151> PRIOR FILING DATE: 1996-05-01
 18 <150> PRIOR APPLICATION NUMBER: 08/761,277
 19 <151> PRIOR FILING DATE: 1996-12-06
 21 <160> NUMBER OF SEQ ID NOS: 80
 23 <170> SOFTWARE: PatentIn version 3.1

25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 28
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Synthetic

33 <400> SEQUENCE: 1
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 40 <213> ORGANISM: Artificial Sequence
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 46 gatccgaatt cggcctccgc ggccgctcta gatgca

49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 677
 51 <212> TYPE: DNA
 52 <213> ORGANISM: SV40 Poly A
 54 <400> SEQUENCE: 3

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 57 aaaaaaatgc tttatttgtg aaatttgtga tgctattgct ttatttgtaa ccattataag 120
 59 ctgcaataaa caagttaaca acaacaattg cattcatttt atgtttcagg ttcaggggga 180
 61 ggtgtgggag gtttttttaa gcaagtaaaa cctctacaaa tgtggtatgg ctgattatga 240
 63 tcatgaacag actgtgagga ctgaggggcc tgaaatgagc cttgggactg tgaatcaatg 300
 65 cctgtttcat gccctgagtc ttccatgttc ttctccccc catcttcatt tttatcagca 360
 67 ttttcctggc tgtcttcac atcatcatca ctgtttctta gccaatctaa aactccaatt 420
 69 cccatagcca cattaaactt cattttttga tacactgaca aactaaactc tttgtccaat 480
 71 ctctctttcc actccacaat tctgctctga atactttgag caaactcagc cacaggctctg 540

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73 taccaaatta acataagaag caaagcaatg ccactttgaa ttattctctt ttctaacaaa      600
75 aactcactgc gttccaggca atgctttaaa taatctttgg gcctaaaaatc tatttgtttt      660
77 acaaactctgg cctgcag                                           677
80 <210> SEQ ID NO: 4
81 <211> LENGTH: 39
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83 <213> ORGANISM: Artificial Sequence
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86 <223> OTHER INFORMATION: Synthetic
88 <400> SEQUENCE: 4
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95 <213> ORGANISM: Artificial Sequence
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105 <211> LENGTH: 633
106 <212> TYPE: DNA
107 <213> ORGANISM: SR alpha promoter
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112 gcagaagtat gcaaagcatg catctcaatt agtcagcaac caggtgtgga aagtccccag      120
114 gctccccagc aggcagaagt atgcaaaagca tgcattctcaa ttagtcagca accatagtcc      180
116 cgcccctaac tccgcccatc ccgccctaa ctccgcccag ttccgcccac tctccgcccc      240
118 atggctgact aatttttttt atttatgcag aggccgaggc cgctcggcc tctgagctat      300
120 tccagaagta gtgaggaggc ttttttgag gcctaggctt ttgcaaaaag ctctcgagc      360
122 tcgcatctct cttcacgcg ccgcgccccc tacctgaggc cgccatccac gccggttgag      420
124 tcgcgttctg ccgcctcccg cctgtggtgc ctctgaact gcgtccgccc tctaggtaag      480
126 tttagagctc aggtcgagac cgggcctttg tccggcgctc cttggagcc tacctagact      540
128 cagccggctc tccacgcttt gcctgaccct gcttgctcaa ctctacgtct ttgtttcgtt      600
130 ttctgttctg cgccgttaca gatcgctcg agg                                           633
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134 <211> LENGTH: 635
135 <212> TYPE: DNA
136 <213> ORGANISM: Moloney LTR virus
138 <400> SEQUENCE: 7
139 caagcttcgc attagtccaa tttgttaaag acaggatata agtgggccag gctctagttt      60
141 tgactcaaca atatcaccag ctgaagccta tagagtacga gccatagata aaataaaaaga      120
143 ttttattttag tctccagaaa aaggggggaa tgaaaagccc cacctgtagg tttggcaagc      180
145 tagcttaagt aacgccattt tgcaaggcat ggaaaaatac ataactgaga atagagaagt      240
147 tcagatcaag gtcaggaaca gatggaacag ctgaatatgg gccaaacagg atatctgtgg      300
149 taagcagttc ctgcccgggc tcagggccaa gaacagatgg aacagctgaa tatgggccaa      360
151 acaggatata tgtggtaagc agttcctgcc ccggtcagg gccaaagaaca gatgggtccc      420
153 agatgcggtc cagccctcag cagtttctag agaaccatca gatgtttcca gggtgcccca      480
155 aggacctgaa atgacctgtg gccttatttg aactaaccaa tcagttcgct tctcgcttct      540

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157 gttcgcgcgc tctgtctccc cgagctcaat aaaagagccc acaaccctc actcggggcg 600
159 ccagtcctcc gattgactga gtcgccccct cgagg 635
162 <210> SEQ ID NO: 8
163 <211> LENGTH: 483
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 8
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170 cctccccgtc accaccccc ccaaccgcc ccgaccggag ctgagagtaa ttcatacaaa 120
172 aggactcgcc cctgccttgg ggaatcccag ggaccgtcgt taaactccca ctaacgtaga 180
174 acccagagat cgctgcgttc ccgccccctc acccgccgc tctcgtcatc actgagggtg 240
176 agaagagcat gcgtgaggct ccggtgccc gtcagtgggca gagcgcacat cgcccacagt 300
178 ccccgagaag ttgggggggag gggtcggcaa ttgaaccggg gcctagagaa ggtggcgcg 360
180 ggtaaaactg gaaagtgatg tcgtgtactg gctccgcctt tttcccgagg gtgggggaga 420
182 accgtatata agtgcagtag tcgccgtgaa cgttctttt cgcaacgggt ttgccgcctc 480
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188 <211> LENGTH: 24
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190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Synthetic
195 <400> SEQUENCE: 9
196 aagctttgga gctaagccag caat 24
199 <210> SEQ ID NO: 10
200 <211> LENGTH: 23
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Synthetic
207 <400> SEQUENCE: 10
208 ctcgaggcgg caaaccggtt gcg 23
211 <210> SEQ ID NO: 11
212 <211> LENGTH: 1451
213 <212> TYPE: DNA
214 <213> ORGANISM: Homo sapiens
216 <400> SEQUENCE: 11
217 aagctttgga gctaagccag caatggtaga gggaagattc tgcacgtccc ttccaggcgg 60
219 cctccccgtc accaccccc ccaaccgcc ccgaccggag ctgagagtaa ttcatacaaa 120
221 aggactcgcc cctgccttgg ggaatcccag ggaccgtcgt taaactccca ctaacgtaga 180
223 acccagagat cgctgcgttc ccgccccctc acccgccgc tctcgtcatc actgagggtg 240
225 agaagagcca tgcgtgaggc tccggtgccc gtcagtgggc agagcgcaca tcgcccacag 300
227 tccccgagaa gttgggggga ggggtcggca attgaaccgg tgcctagaga aggtggcgcg 360
229 gggtaaaactg ggaaagtgat gtcgtgtact ggctccgctt ttttcccgag ggtgggggag 420
231 aaccgtata taagtgcagt agtcgccgtg aacgttctt ttcgcaacgg gtttgccgcc 480
233 agaacacagg taagtgcgt gtgtggttcc cgcgggcctg gcctctttac gggttatggc 540
235 ccttgcgtgc cttgaattac ttccacgcc ctggctgcag tacgtgattc ttgatcccga 600
237 gcttcggggtt ggaagtgggt gggagagttc gaggccttg gcttaaggag ccccttcgcc 660
239 tcgtgcttga gttgaggcct ggcctgggcg ctggggcccc cgctgcgaa tctggtggca 720

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241 ccttcgcgcc tgtctcgtcg ctttcgataa gtctctagcc atttaaaatt tttgatgacc 780
243 tgctgcgacg ctttttttct ggcaagatag tcttgtaaatt gcgggcccaag atctgcacac 840
245 tggattttcg gtttttgggg ccgcggggcg cgacggggcc cgtgcgtccc agcgcacatg 900
247 ttcggcgagg cggggcctgc gagcgcggcc accgagaatc ggacgggggt agtctcaagc 960
249 tggccggcct gctctggtgc ctggcctcgc gccgccgtgt atcgccccgc cctggggcggc 1020
251 aaggctggcc cggtcggcac cagttgcgtg agcggaaaga tggccgcttc ccggccctgc 1080
253 tgcagggagc tcaaaatgga ggacgcggcg ctccgggagag cgggcgggtg agtcacccac 1140
255 acaaaggaaa agggcccttc cgtcctcagc cgtcgcttca tgtgactcca cggagtaccg 1200
257 ggcccgctcc aggcacctcg attagtcttc gagcttttgg agtacgtcgt ctttaggttg 1260
259 gggggagggg ttttatgcga tggagtttcc ccacactgag tgggtggaga ctgaagttag 1320
261 gccagcttgg cacttgatgt aattctcctt ggaatttgcc ctttttgagt ttggatcttg 1380
263 gttcattctc aagcctcaga cagtggttca aagttttttt cttccatttc aggtgtcgtg 1440
265 aaaactctag a 1451
268 <210> SEQ ID NO: 12
269 <211> LENGTH: 23
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Synthetic
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280 <210> SEQ ID NO: 13
281 <211> LENGTH: 1289
282 <212> TYPE: DNA
283 <213> ORGANISM: Mus musculus
285 <220> FEATURE:
286 <221> NAME/KEY: CDS
287 <222> LOCATION: (88)..(741)
288 <223> OTHER INFORMATION:
291 <400> SEQUENCE: 13
292 ttacctcaact gctttccgga gcggtagcac ctctcccgcc ggcttccctcc tcagaccgct 60
294 ttttgccgcg agccgaccgg tcccgtc atg ccg acc cgc agt ccc agc gtc gtg 114
295 Met Pro Thr Arg Ser Pro Ser Val Val
296 1 5
298 att agc gat gat gaa cca ggt tat gac cta gat ttg ttt tgt ata cct 162
299 Ile Ser Asp Asp Glu Pro Gly Tyr Asp Leu Asp Leu Phe Cys Ile Pro
300 10 15 20 25
302 aat cat tat gcc gag gat ttg gaa aaa gtg ttt att cct cat gga ctg 210
303 Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly Leu
304 30 35 40
306 att atg gac agg act gaa aga ctt gct cga gat gtc atg aag gag atg 258
307 Ile Met Asp Arg Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu Met
308 45 50 55
310 gga ggc cat cac att gtg gcc ctc tgt gtg ctc aag ggg ggc tat aag 306
311 Gly Gly His His Ile Val Ala Leu Cys Val Leu Lys Gly Gly Tyr Lys
312 60 65 70
314 ttc ttt gct gac ctg ctg gat tac att aaa gca ctg aat aga aat agt 354
315 Phe Phe Ala Asp Leu Leu Asp Tyr Ile Lys Ala Leu Asn Arg Asn Ser
316 75 80 85

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318 gat aga tcc att cct atg act gta gat ttt atc aga ctg aag agc tac      402
319 Asp Arg Ser Ile Pro Met Thr Val Asp Phe Ile Arg Leu Lys Ser Tyr
320 90                               95                               100                               105
322 tgt aat gat cag tca acg ggg gac ata aaa gtt att ggt gga gat gat      450
323 Cys Asn Asp Gln Ser Thr Gly Asp Ile Lys Val Ile Gly Gly Asp Asp
324                               110                               115                               120
326 ctc tca act tta act gga aag aat gtc ttg att gtt gaa gat ata att      498
327 Leu Ser Thr Leu Thr Gly Lys Asn Val Leu Ile Val Glu Asp Ile Ile
328                               125                               130                               135
330 gac act ggt aaa aca atg caa act ttg ctt tcc ctg gtt aag cag tac      546
331 Asp Thr Gly Lys Thr Met Gln Thr Leu Leu Ser Leu Val Lys Gln Tyr
332                               140                               145                               150
334 agc ccc aaa atg gtt aag gtt gca agc ttg ctg gtg aaa agg acc tct      594
335 Ser Pro Lys Met Val Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser
336                               155                               160                               165
338 cga agt gtt gga tac agg cca gac ttt gtt gga ttt gaa att cca gac      642
339 Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro Asp
340 170                               175                               180                               185
342 aag ttt gtt gtt gga tat gcc ctt gac tat aat gag tac ttc agg aat      690
343 Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asn
344                               190                               195                               200
346 ttg aat cac gtt tgt gtc att agt gaa act gga aaa gcc aaa tac aaa      738
347 Leu Asn His Val Cys Val Ile Ser Glu Thr Gly Lys Ala Lys Tyr Lys
348                               205                               210                               215
350 gcc taagatgagc gcaagttgaa tctgcaaata cgaggagtcc tgttgatggt      791
351 Ala
354 gccagtaaaa ttatgcaggtg ttctagtcct gtggccatct gcctagtaaa gcttttttgca      851
356 tgaacctttct atgaatgtta ctgtttttatt tttagaaatg tcagtttgctg cgtccccaga      911
358 cttttgatttt gcactatgag cctataggcc agcctaccct ctggttagatt gtcgcttatt      971
360 ttgtaagaaa aacaaatctc ttaaattacc actttttaaat aataataactg agattgtatc      1031
362 tgtaagaagg atttaagag aagctatatt agtttttttaa ttggtattttt aattttttata      1091
364 tattcaggag agaaagatgt gattgatatt gttaatttag acgagtctga agctctcgat      1151
366 ttcctatcag taacagcatc taagaggttt tgctcagtgg aataaacatg tttcagcagt      1211
368 gttggctgta ttttcccact ttcagtaaat cgttgtcaac agttcctttt aaatgcaaat      1271
370 aaataaattc taaaaatt                                     1289
373 <210> SEQ ID NO: 14
374 <211> LENGTH: 218
375 <212> TYPE: PRT
376 <213> ORGANISM: Mus musculus
378 <400> SEQUENCE: 14
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381 1                               5                               10                               15
384 Tyr Asp Leu Asp Leu Phe Cys Ile Pro Asn His Tyr Ala Glu Asp Leu
385                               20                               25                               30
388 Glu Lys Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg
389                               35                               40                               45
392 Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
393                               50                               55                               60
396 Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:1988 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80